

## FIG. IA-I

FIG. IA-2 Pro-peptide

EQDVDLQKYLEKYYNLKNDGROVEKRRNSGPVV-EKLKQMQUEFFGLKVTGKP  
 79  
 DVAPK-TDEKELAVQYLNTF-YGCPKE-SCNLFVILKDTLKKMOKFFGLPQTGDL  
 89  
 79  
 DTSMNLVQKYLENYDLKKDVKQFVRRKDSCPVV-KKIREMOKEFGLLEVTKL  
 79  
 AGGMSELQWEQAQDY-LKRFYLYDSETKNANSLE-AKLKEMQKFFGLPITGML  
 74  
 EKNTKTVQDYLEKFYOLPSNQYQSTR-KNGTNVIVEKLKEMQRFFGLNVTGKP  
 78  
 DLRTNLTDRLQAEEYLYRYGYTRVAEMRGESKSLSGPALLLQKQQLSLPETGEL  
 86  
 DSNKDLAQQYLEKYYNLKDVQFRRK-DSNLIV-KKIQGMQKFLGLEVTGKL  
 78  
 67  
 PDVHHLHAERRGPQ-----PWHAALPSSPAPAPATQE  
 79  
 KNNVLFGERYLEKFYGLEINKLPVTKMKYSGNIMKEKIQEMQHFLGLKVTGQL  
 79  
 -----EAWLQOQYGYLPPGDLRTHTQRSQPSLS-AAIAAMQKFYGLOVTGKA  
 80  
 88  
 TEQYFNVEWLQKYGYLPPTSRMSVVRSAETMQ-SALAAAMQQFYGINMTGKV  
 100  
 .KL..MQKF.GL.VTCKL

Catalytic

YRIENYTPDLPRADVDAIEKAFQLWSNVTPLTFTKV-----SEGQADIM  
YRIIGYTPDLDPETVDDAFAFARAQVWSNVTPLRFsRI-----HDGEADIM  
YRIVNYTPDLPKDAVDSAVEKALKVWEEVTPLTFSRL-----YEGEADIM  
YRIVSYTROLPHITVDRILWSKALNMWKGKEIPLHFRKV-----VWGTADIM  
YRIRNYTPQOLSEAEVERAIKDAFELWSVASPLIFTRI-----SQGEADIN  
YWIQNYSEDLPRAVDDAFAFALAFLWSAVTPLTFTRV-----YSRDAIV  
YRIVNYTPDLPRDAVDSATEKALKVWEEVTPLTFSRL-----YEGEADIM  
YRILREPWQLVQEQRQTMAEAALKVWSNVTPLTFTEV-----HEGRADIM  
YRINNYTPDMNREDDVDYAIRKAFOQVWSNVTPLKFSKI-----NTGMADIL  
FCIONNYTPKVGEYATYEAIRKAFRVWEATPLRFREVVPYAYIREGHEKQADIM  
YSIKNVTPKVGDPETRKAIRRAFDVWQNTPLTFFEEVPYSELENGK-RDVDIP  
YRINNYTPDLSVVD-AI-KAF-VWS-VTPLTF::V-----G.ADIM  
160 170 160 155 159 167 159 156 160 178 185 200

## FIG. 1B-1

### Catalytic

MMP-1  
MMP-2  
MMP-3  
MMP-7  
MMP-8  
MMP-9  
MMP-10  
MMP-11  
MMP-12  
MT-MMP-1  
MT-MMP-3  
Consensus

ISFVRCGDHRDMSPFDCPGGNILAHAFQPGPGIGGDAHFDEHERWTN-NFTEYN  
INFGRWEHGDCGYPFDCGKDGGLILAHAFAPGTVGGDSHFDDDELWTLGEQVVR  
ISFAVREHGDFYPFDCPGNVILAHAFAPGPGINGDAHFDDDEQWTK-DTTGTN  
IGFARGAHGDSYPFDCPGNTILAHAFAPGTGLGGDAHFDEDERWTDGSSLGIN  
IAFYQRDHGDNNSPFDCPGNGILAHAFQPGQGIGGDAHFDAEETWTN-TSANYN  
IQFGVVAEHGDGYPFDCGKDGGLILAHAFPPGPGLQGDAHFDDDEKWT-EASGTN  
ISFAVKEHGDFYSFDCPGHSILAHAYPPGPGLYCDIHFDDEKWT-DASGTN  
IDFARYWDGDDLPFDGPGGILAHAFFPKTHREGDVHFDYDETWТИGDDQGTD  
VVFARGAHGDFHAFDGKGGILAHAFPGSGIGGDAHFDEDEFWT-HSGGTN  
IFFAEGFHGDSTPFDCEGGFILAHAYPEPGPNIGGDTHFDSAEPWTV-RNEDLN  
IIFASGFHGDSSSPFDCEGGFILAHAYPEPGPGIGGDTHFDSDEPWTLGNPNHDG  
I.FA...HGD..PFDGPGG.LAHAF.PGPGIGGDAHF.DE.WT.-...N

### Catalytic

MMP-1  
MMP-2  
MMP-3  
MMP-7  
MMP-8  
MMP-9  
MMP-10  
MMP-11  
MMP-12  
MT-MMP-1  
MT-MMP-3  
Consensus

-----  
YGFCPHEALFTMGGNAEGQPKFPRFQGTSYDSCTTEGRTDGYRWCGTTED  
-----  
-----  
-----  
-----  
FGFCPSERLYTRDGNADGXPCQFPFIQGQSYSACTTDGRSDGYRWCAATTAN  
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## FIG. IB-2

VKYGNADGEYCKFPFLFNGKEYNSCTDTGRSDGFLWCSTTYNFEKDGK	211
-----	211
-----	207
-----	210
TRFGNADGACHEPFIFEGRSYSACTIDGRSDGLPWHCSTTANYDIDDDR	267
-----	210
-----	208
-----	211
-----	229
-----	237
-----	300

YDRDKKYGFCPETAMSTV-GGNSEGAPCVFPETFLGNKYESCTSAGRS 369  
211  
211  
207  
210  
210  
208  
211  
229  
237  
400

## FIG. IC-1

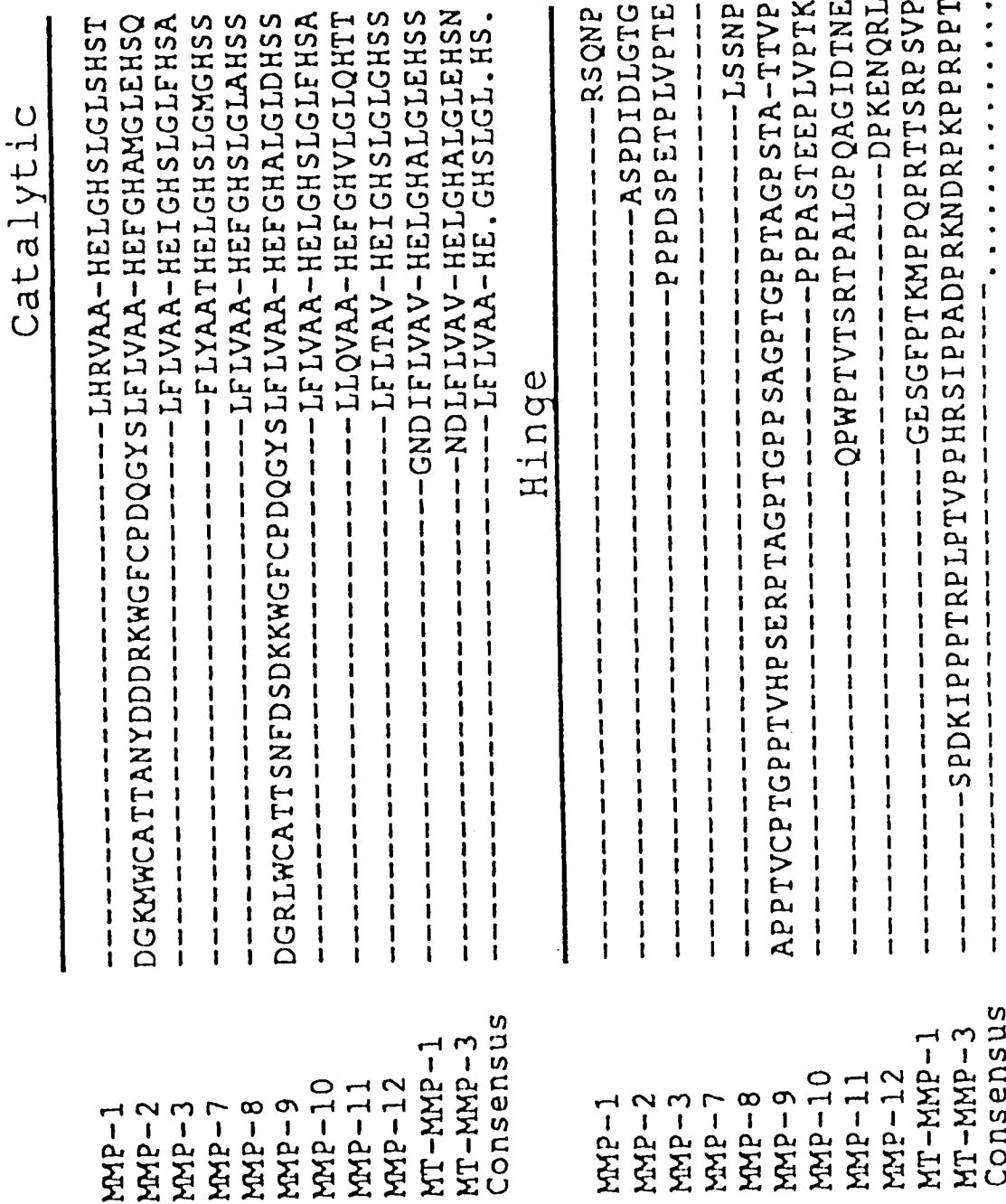
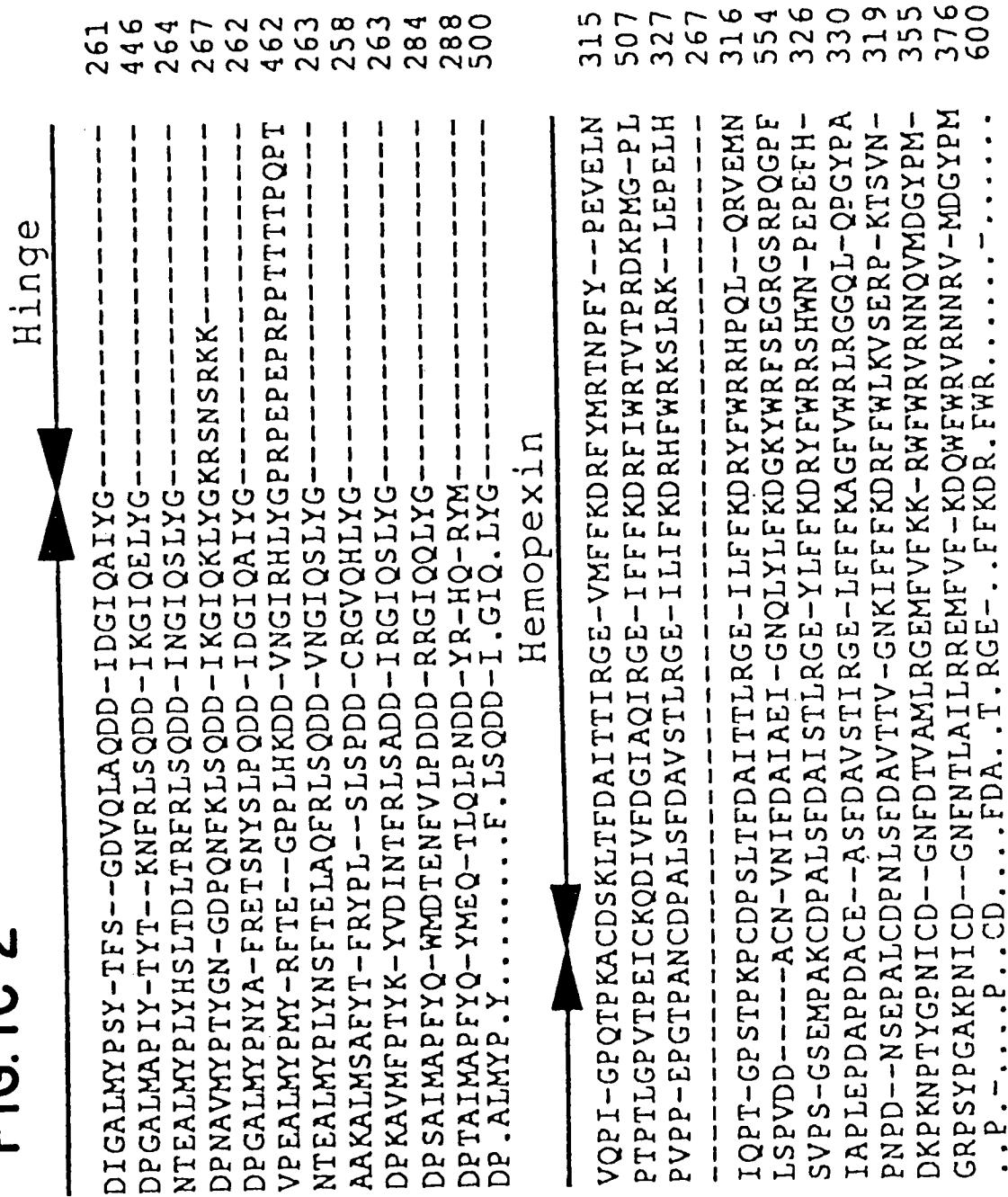


FIG. IC-2



## FIG. 1D-1

### Hemopexin

MMP-1	FTSVFWPQLPQNGLEAAAYEFA	DRDEVRF	FKGNKYAV	-QGQNVLHGY	PKDIYSSEFGFPR
MMP-2	LVATEFWPELPEKIDAVYEAPQEE	KAVF	FAGNEYWIY	-SASTLERGYP	KPLTS-LGLPP
MMP-3	LISSFWPSLPSGVDAAYEVTS	KDLDVF	FKGNQFWAI	-RGNEVRAGYPRGIH	-LGFP
MMP-7					
MMP-8	FISLFWPSLPTGIQAAAYEDFD	RDLIF	FKGNQYWA	-SGYDILQGYPKDISN-YGFPS	
MMP-9	LIADDKWPALPRKLD	SVFEEPLSKL	FFFSGRQVWVYT	GASVL-G-PRRLDK-LGLGA	
MMP-10	LISAFWP	SILPSYLDAA	YEVNSRDTVF	IIFKGNEFWAI-RGNEVQAGYPRGIH	-LGFP
MMP-11	LA	SRRHWAQGLPSPVDA	DAFE-DAQGH	IWEFQGAQYVY-DGEKPVLG-PAPL	TE-LGLVR
MMP-12	LISSLW	WP	TLPSGIEAAYEIEARN	QVFLFKDDKYWLI-SNLRPEPNPKSIHS-FGFP	N
MT-MMP-1	PIQGFWRGLPASINTAYER	KDGKFVF	-FKGDKH	VVF-DEASLEPGYPKHIKE-LGRGL	
MT-MMP-3	QITYFWRGLPPSIDAVYEN	SDGNFVF	-FKGNKYAVF-KDTTLQPGYPHD	LIT-LGSGI	
Consensus	LIS.FWP.	LP...	DAAYE...	...VF.FKGN.YW...	-LG.P.

### Hemopexin

MMP-1	MIAHDFPGIGHKVDAVFMKD	GFF	--YFFHGTRQYKFD	PKT-KRILTL-QKANS-WFNC
MMP-2	LIADAWNAPIPDNLDAVVLQ	GGGHSYFFKGAYYLKLENQS	-LKSVKF-GSIKSDWLGC	
MMP-3	QIAEDFPGIDSKIDAVFEEFG	FF--YFFTGS	SSQLEFDNA-KKVTHT-LKSNS-WLNC	
MMP-7	SISGAFPGIESKVD	DAVFQQE	HVFSGPRYYAFDLIA-QRVTRV-ARGNK-WLNC	
MMP-8	EVDRMFPGVPLDTHDVFQY	REKA--YFCQDRFYWRVSSRSELNQVDQVGYVTYDILQC		
MMP-9	LIADDDFPGVEPKVDAVLQAF	GFF--YFFSGSSQFEEDPNA-RMVTHI-LKSNS-WLHC		
MMP-10	R-ATDWRGVPSEIDAAFQDAD	GYA-YFLRGRLYWKFDPVK-VKALEGFPRLVGP	DFFG	
MMP-11	LITKNFQGIGPKIDAVFSK	NQFEYDFLL-QRITKT-LKSNS-WFGC		
MMP-12	NIKVWE-GIPESPRGSEMG	SDEVFYFYKGNKYWKFN	NQKLKVEPGYPKSALRDWMGC	
MT-MMP-1	PITVWK-GIPESPQGAFVH	KENGFTYFKEGVILEIQTTRY	SRIEPEGHPRSLKDLSSGC	
MT-MMP-3	I...F.GI...DAVF	--YFF.G...FD...	-W..C	
Consensus				

FIG. ID-2

TVKHIDAA-LSEENTGKTYFFVANKYWRYDEYKRSMDPGYPK	413
DVQRVDAA-FNWSKNNKTYIFAGDKFWRYNEVKKMDPGFPK	604
TVRKIDAA-ISDKEKNKTYFFVEDKYWRFDEKRN SMEPGFPK	424
	267
SVQAIIDAA-VFYRS--KTYFFVNDQFWRYDNQRQFMEPGYPK	411
DVAQVTGA-LRSGR-GKMLLFSGRRILWRFDVKAQMVDPRSAS	648
TIRKIDAA-VSDKEKKKTYFFAADDKYWRFDENQSMEQGFPR	423
FP--VHAALLVWGP EKNNKTYFFRGRDYWRFHPSSTRRVDSVPR	424
FVKIDAA-VENP RFYRTYFFVDNQYWRYDERRQMMDPGYPK	416
PTDKIDAA-LFWMMPNGKTYFFRGNKYYRFNEELRAVDSEYPK	451
PPHGIDSA-IWWEDVUGKTYFFKGDRYWRYSEEMKTMDPGYPK	472
.V..IDAA-.....KTYFF.....YWR.DE....MDPG.PK	700
RKN-----	469
	660
	477
	267
RYG-----	467
PED-----	707
CAEPANTFL-----	476
	488
	470
PSGGRPDEGTEEEETE-VIIIEEGGGAVSAAVVLPVLL	549
DGPTDRVKEGHSPDDVDIVKLDNTASTVKAIAVIPCILA	571
	800

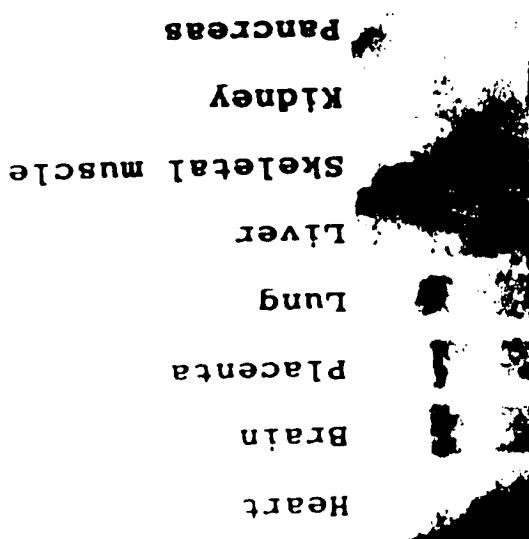
## FIG. 1E

MMP-1	469
MMP-2	660
MMP-3	477
MMP-7	267
MMP-8	468
MMP-9	708
MMP-10	476
MMP-11	489
MMP-12	470
MT-MMP-1	582
MT-MMP-3	604
Consensus	833

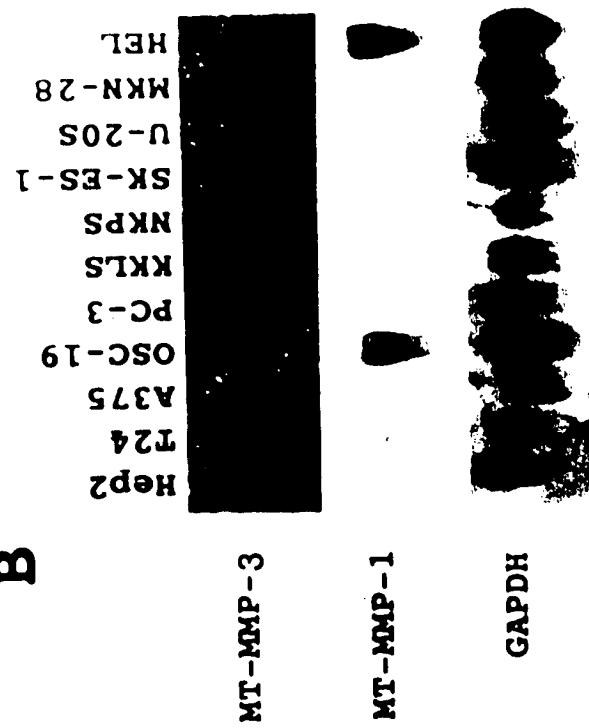
LLVIAVGLAVFFRRHGTPRRLIYCQRSLLDKV  
LCLLVLYTVFQFKRKGTPRHILYCKRSMQEWV

# FIG. 2

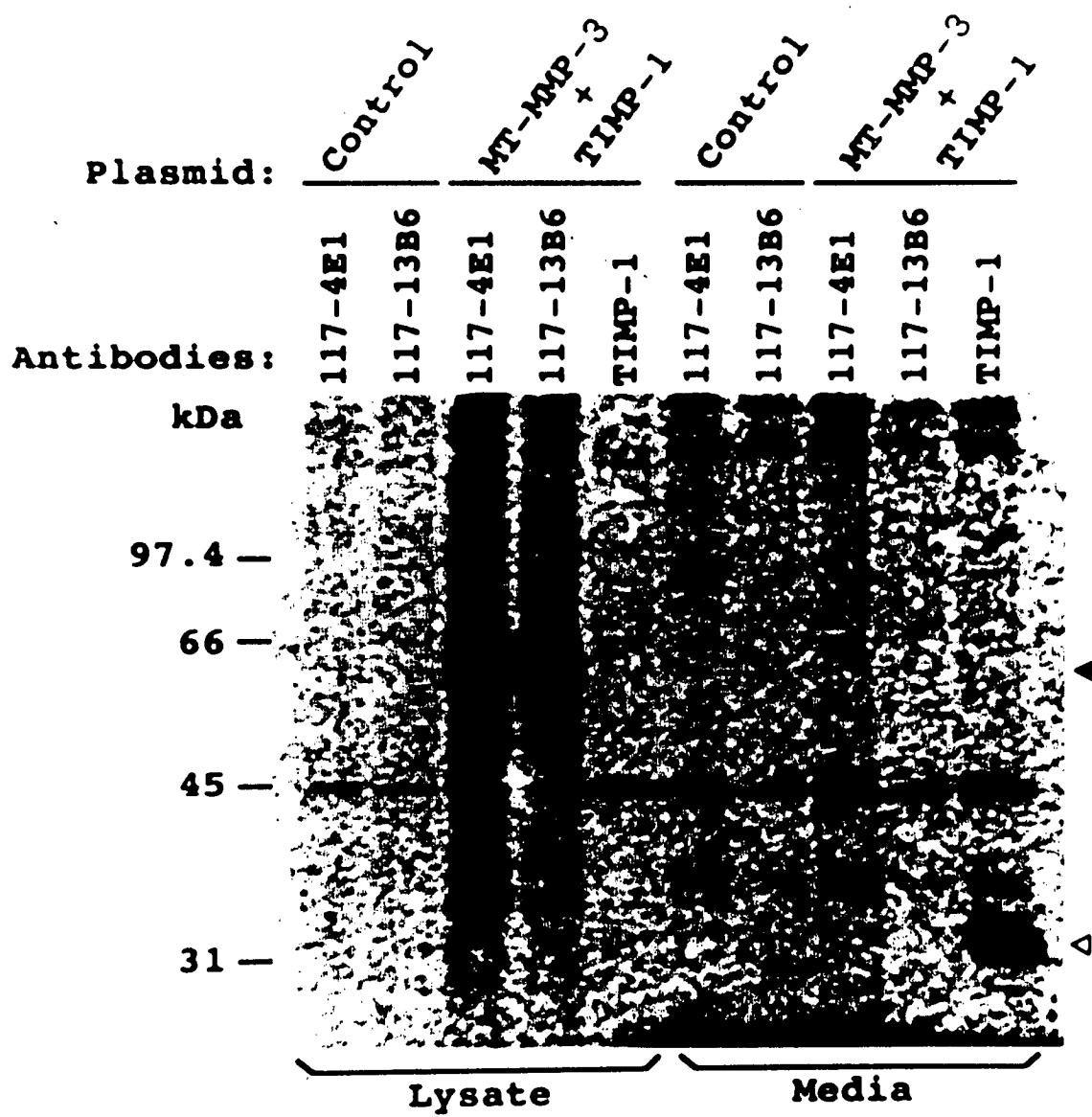
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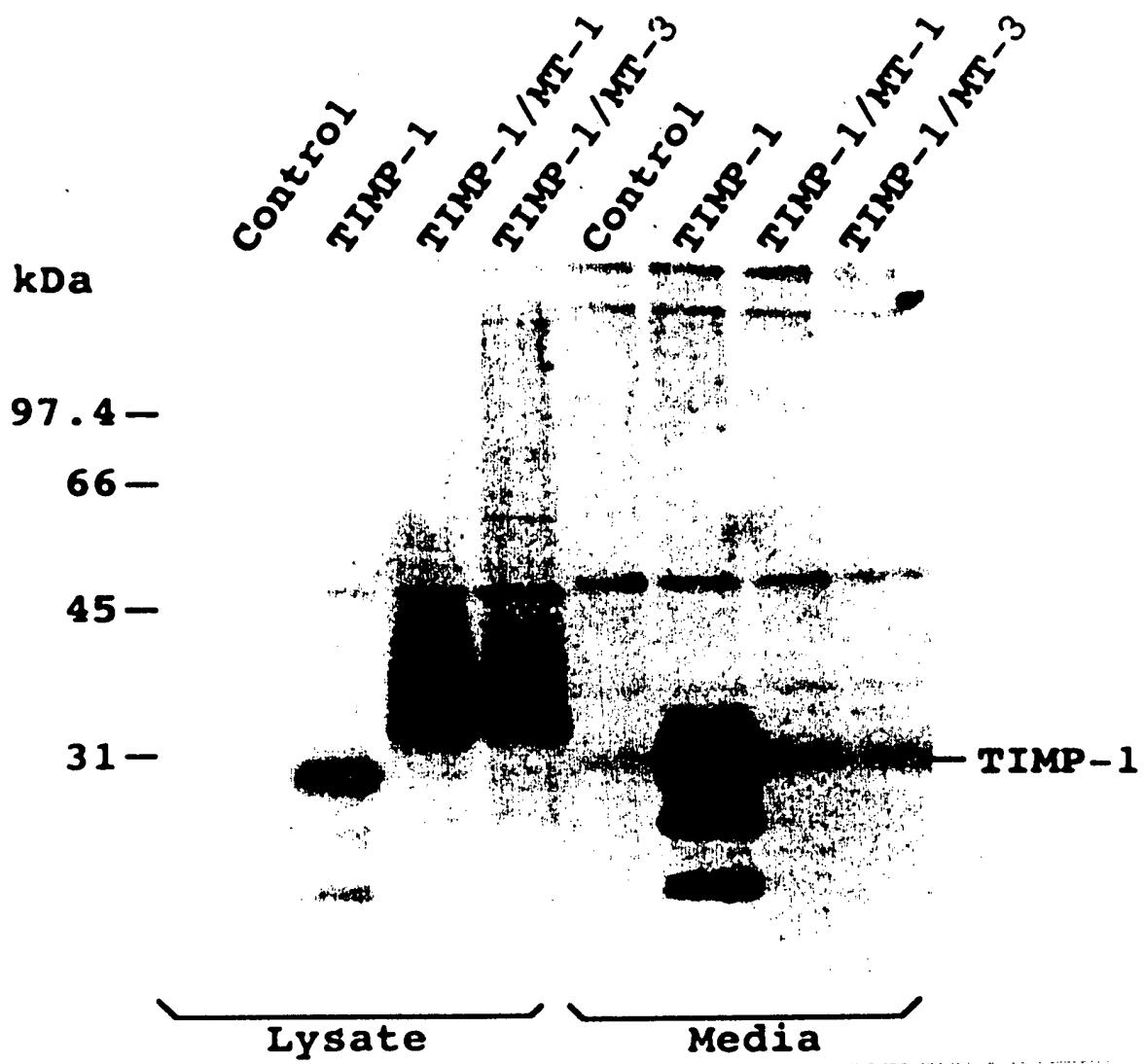
B



**FIG. 3**



**FIG. 4**



5  
FIG.

## Control

TIME-1/MT-3

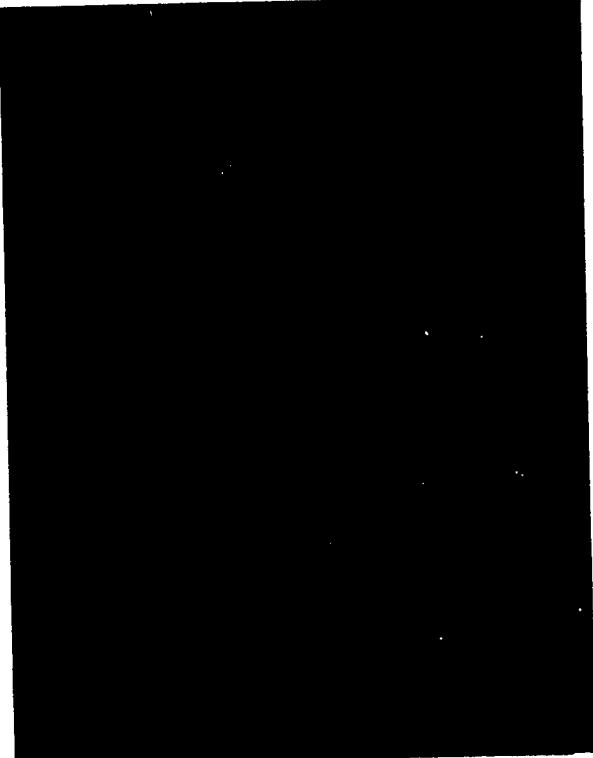


FIG. 6

